Dynamics of biological systems: from viruses to populations

Contribution ID: 10

Type: not specified

## **Building clone-consistent ecosystem models**

Wednesday 23 September 2020 16:05 (20 minutes)

Many ecological studies employ general models that can feature an arbitrary number of populations. A common requirement imposed on such models is what we call *clone consistency*: If the individuals from two populations are indistinguishable, joining these populations into one shall not affect the outcome of the model. Otherwise a model produces different outcomes for the same scenario. Using functional analysis, we comprehensively characterize all clone-consistent models: We prove that they are necessarily composed from basic building blocks, namely linear combinations of parameters and abundances. These strong constraints enable a straightforward validation of model consistency or reveal implicit assumptions required to achieve it. Moreover, our insights facilitate building new clone-consistent models, which we illustrate for a data-driven model of microbial communities.

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Session Classification: Afternoon Session